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## **Prostaglandin F2 promotes embryo implantation and development in the pig**

Kaczyński, Piotr ; Baryła, Monika ; Goryszewska, Ewelina ; Bauersachs, Stefan ; Wacławik, Agnieszka

**Abstract:** Successful establishment and development of pregnancy requires proper communication between developing conceptuses and the maternal reproductive tract. Prostaglandins are key players involved in the regulation of reproductive processes in mammals including pigs. Due to its luteolytic action, prostaglandin F2- $\alpha$  (PGF2) is mainly considered as an undesirable factor during early pregnancy. However, its content in the uterine lumen is elevated in pigs and other mammals. Recently, we reported an important role of PGF2 in the endometrium during early pregnancy in the pig. Thus, the aim of the present study was to determine whether PGF2 can act on porcine trophoblast and if so, to elucidate what effect it could exert. We detected increased expression of PGF2 receptor during the implantation period (from day 14 until day 19 of pregnancy). Global gene expression profiling using microarrays and quantitative PCR studies revealed that PGF2 acting on porcine trophoblast cells in vitro alters expression of genes potentially involved in processes related to implantation, such as: cell proliferation, focal adhesion, extracellular matrix binding, cell migration, cytoskeleton organization, immune interactions, ion homeostasis, and lipid metabolism. Using primary porcine trophoblast cells, we demonstrated that PGF2 stimulated trophoblast cell proliferation and adhesion to extracellular matrix protein. This was likely mediated by mitogen-activated protein kinases (MAPK1/3) and focal adhesion kinase (FAK) since we observed increased phosphorylation of MAPK1/3 and FAK in trophoblast cells treated with PGF2. To conclude, the present report indicates a novel role for PGF2 in the porcine conceptus as a para- and autocrine factor supporting pregnancy establishment.

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1    **TITLE**

2    Prostaglandin F2 $\alpha$  promotes embryo implantation and development in the pig

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10   **SHORT TITLE**

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## ABSTRACT

Successful establishment and development of pregnancy requires proper communication between developing conceptuses and the maternal reproductive tract. Prostaglandins are key players involved in the regulation of reproductive processes in mammals including pigs. Due to its luteolytic action, prostaglandin F<sub>2</sub>-alpha (PGF<sub>2</sub> $\alpha$ ) is mainly considered as an undesirable factor during early pregnancy. However, its content in the uterine lumen is elevated in pigs and other mammals. Recently, we reported an important role of PGF<sub>2</sub> $\alpha$  in the endometrium during early pregnancy in the pig. Thus, the aim of the present study was to determine whether PGF<sub>2</sub> $\alpha$  can act on porcine trophoblast and if so, to elucidate what effect it could exert. We detected increased expression of PGF<sub>2</sub> $\alpha$  receptor during the implantation period (from day 14 until day 19 of pregnancy). Global gene expression profiling using microarrays and quantitative PCR studies revealed that PGF<sub>2</sub> $\alpha$  acting on porcine trophoblast cells in vitro alters expression of genes potentially involved in processes related to implantation, such as: cell proliferation, focal adhesion, extracellular matrix binding, cell migration, cytoskeleton organization, immune interactions, ion homeostasis, and lipid metabolism. Using primary porcine trophoblast cells, we demonstrated that PGF<sub>2</sub> $\alpha$  stimulated trophoblast cell proliferation and adhesion to extracellular matrix protein. This was likely mediated by mitogen-activated protein kinases (MAPK1/3) and focal adhesion kinase (FAK) since we observed increased phosphorylation of MAPK1/3 and FAK in trophoblast cells treated with PGF<sub>2</sub> $\alpha$ . To conclude, the present report indicates a novel role for PGF<sub>2</sub> $\alpha$  in the porcine conceptus as a para- and autocrine factor supporting pregnancy establishment.

43

44 **Introduction**

45 The establishment and development of pregnancy in the pig, as in any mammalian species,  
46 requires proper communication between developing conceptuses and the intrauterine  
47 environment. This embryo-maternal dialog includes hormonal and immune interactions precisely  
48 controlled by hormones, cytokines, growth factors and other molecules interacting in endo-,  
49 para- and autocrine manners.

50 During the maternal recognition of pregnancy period, which occurs in pigs on days 11-12 of  
51 pregnancy, conceptuses secrete increased levels of estrogens that are one of the major conceptus  
52 signals for the establishment of pregnancy. This leads to the redirection of luteolytic  
53 prostaglandin F2 $\alpha$  (PGF2 $\alpha$ ) secretion from endocrine to exocrine (to the uterine lumen) mode,  
54 and also affects the hormonal environment in the reproductive tract, resulting in prolonged  
55 lifespan of the corpus luteum (CL) and, thereby, maintained progesterone (P4) synthesis (Bazer  
56 & Thatcher 1977). The second phase of increased estrogen secretion occurs in pigs on day 15 of  
57 pregnancy and lasts until day 25 after fertilization (Geisert *et al.* 1990).

58 Key factors involved in the control of reproductive processes in mammals are prostaglandins  
59 (PGs). Their importance for pregnancy establishment and development is shown by the fact that  
60 lack of PG synthesis leads to termination of pregnancy just before the implantation process in  
61 mammals such as pigs (Kraeling *et al.* 1985), cattle (Erdem & Guzeloglu 2010) and rodents  
62 (Kennedy *et al.* 2007). Interestingly, intrauterine administration of prostaglandin synthase  
63 inhibitors resulted in improper conceptus elongation in sheep (Dorniak *et al.* 2011) which has a  
64 much different programming for conceptus growth compared to rapid trophoblast elongation in

65 the pig. In contrast, PG synthesis inhibition does not affect elongation of porcine conceptuses  
 66 (Geisert *et al.* 1986) but it does affect their survival during the attachment period (Kraeling *et al.*  
 67 1985). Prostaglandin E2 (PGE2) and PGF2 $\alpha$  are the major prostaglandins involved in  
 68 reproductive functions in mammalian reproductive tracts. They act through their receptors:  
 69 PTGER1-4 (PGE2 receptors isoforms 1-4) and PTGFR (PGF2 $\alpha$  receptor). The expression  
 70 profiles of PTGER2 and PTGER4 were determined in porcine trophoblasts at different stages of  
 71 development (Waclawik *et al.* 2013). However, the expression profile of PTGFR in porcine  
 72 conceptuses during early pregnancy has not been studied yet. Interestingly, the expression of  
 73 PGE2 and PGF2 $\alpha$  synthases is elevated both in porcine endometrium and in conceptuses during  
 74 the maternal recognition of pregnancy and/or implantation (Waclawik *et al.* 2006, Waclawik &  
 75 Ziecik 2007). PGE2 has been described as playing a luteoprotective/luteotrophic role (Waclawik  
 76 *et al.* 2009, Waclawik *et al.* 2008, Waclawik 2011) whereas PGF2 $\alpha$  has been mainly perceived  
 77 as a luteolytic factor in sheep, cattle and pigs, as well as in rats, rabbit and hamsters (reviewed in  
 78 McCracken *et al.* 1999). Thus, it could have also a detrimental effect in pregnancy development  
 79 in mammals, including human, cattle, pigs and dogs (reviewed in Kaczynski *et al.* 2016).  
 80 However, it should not be regarded as undesirable factor in pregnancy because elevated amounts  
 81 of PGF2 $\alpha$  in the uterine lumen and/or its increased endometrial synthesis occur not only in pigs  
 82 (Waclawik *et al.* 2006, Zavy *et al.* 1980) but also in other mammals including rodents, cattle,  
 83 dogs and humans (Kennedy *et al.* 2007, Ulbrich *et al.* 2009, Wang *et al.* 2010, Kowalewski *et al.*  
 84 2014, Vilella *et al.* 2013). Moreover, a novel role for PGF2 $\alpha$  in the porcine endometrium during  
 85 the peri-implantation period has been recently reported by our group, indicating that PGF2 $\alpha$   
 86 participates in pregnancy establishment by promoting angiogenesis and expression of genes

87 involved in endometrial remodeling and embryo-maternal communication (Kaczynski *et al.*  
88 2016).

89 Previously we indicated that synthesis of PGF2 $\alpha$  during the implantation period is elevated both  
90 in the porcine endometrium and the conceptus (Waclawik *et al.* 2006, Waclawik & Ziecik 2007)  
91 Recently we also elucidated the mechanism of PGF2 $\alpha$  action in the endometrium (Kaczynski &  
92 Waclawik 2013; Kaczynski *et al.* 2016). Hence, the question arose whether PGF2 $\alpha$  can act  
93 through its receptor in the conceptus and if so, what could be the role of PGF2 $\alpha$  in porcine  
94 trophoblast cells? During the period when the endometrium becomes receptive for embryo  
95 implantation, both the uterine luminal epithelium and conceptus cells simultaneously initiate the  
96 adhesion cascade (Geisert *et al.* 2015). Attachment of trophoblast cells to luminal epithelium is  
97 supported by interactions between integrins and extracellular matrix (ECM) proteins. Integrin  
98 receptors (AVB1, AVB3, AVB5 and A4B1) are able to bind to the RGD (Arg-Gly-Asp)  
99 sequence present in osteopontin, fibronectin and vitronectin proteins (Bowen *et al.* 1996,  
100 Johnson *et al.* 2003). Our studies indicate the important role of PGE2 in activation of  
101 intracellular pathways in porcine trophoblast cells related to adhesion (mitogen activated protein  
102 kinases 1/3 - MAPK1/3; focal adhesion kinase (FAK) and intracellular adhesion molecule 1  
103 (ICAM1) and promotion of trophoblast adhesion to extracellular matrix (ECM) proteins  
104 (Waclawik *et al.* 2013). Moreover, we demonstrated a stimulatory effect of PGE2 on trophoblast  
105 cell estradiol-17 $\beta$  synthesis (Waclawik *et al.* 2013). It has been shown that lack of PGs (PGE2  
106 and PGF2 $\alpha$ ) decreased adhesion of mouse blastocysts and JEG-3 spheroids to human luminal  
107 epithelial cells (Vilella *et al.* 2013). However, the mechanisms by which PGF2 $\alpha$  may stimulate  
108 trophoblast cell adhesion to ECM proteins remain unknown. Furthermore, despite elevated

conceptus and endometrial synthesis of PGF2 $\alpha$ , its role in the proliferative capacities of trophoblast cells and activation of intracellular pathways is still unresolved.

Based on data in the literature including results from our previous studies, we hypothesized that during early pregnancy in the pig, PGF2 $\alpha$  acting through its receptor in trophoblast cells activates intracellular pathways important for the implantation process. Thus, the objectives of the present study were: (i) to determine the expression profile of the PTGFR gene and protein in porcine conceptuses/trophoblasts at different stages of development; (ii) to investigate the effect of PGF2 $\alpha$  on global gene expression profiles in porcine primary trophoblast cells in vitro; (iii) to study the effect of PGF2 $\alpha$  on trophoblast cell adhesion and proliferation; and (iv) to evaluate whether PGF2 $\alpha$  may activate MAPK1/3 and FAK in porcine trophoblast cells, which could be involved in adhesion and/or proliferation processes .

## **MATERIALS AND METHODS**

All procedures involving animals were conducted in accordance with the national guidelines for agricultural animal care and were approved by the Animal Ethics Committee, University of Warmia and Mazury in Olsztyn, Poland, permission No. 36/2012.

### **Experiment 1: PTGFR mRNA and protein expression in the porcine conceptus/trophoblast.**

Gilts after two natural estrous cycles were bred at the onset of estrus (day 0) and then 12 h and 24 h later. Pregnant gilts were slaughtered at the local abattoir. Conceptuses at the pre-implantation stage were flushed from the uterine horns with 20 mL of sterile phosphate-buffered saline (PBS; 137 mM NaCl, 27 mM KCl, 10 mM Na<sub>2</sub>HPO<sub>4</sub> and 2 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.4). Conceptuses/trophoblasts at the implantation and early placentation stage were dissected from the endometrium. Considering the days of pregnancy and morphology of trophoblasts, the

conceptus samples derived from the same animal were pooled and classified into the following groups: days 10-12 (preimplantation stage; spherical and tubular forms, n=5), days 14-15 (beginning of attachment/implantation; filamentous forms, n=5), days 16-19 (filamentous forms; implantation stage, n=7) and days 20-25 (chorion which originates from trophoblast; the onset of placenta development; n=10). Dissections of trophoblast tissues from conceptuses was performed since day 18 post mating (Waclawik *et al.* 2013). Therefore, expression of PTGFR was analyzed in 10- to 17-day conceptuses and 18- to 25-day trophoblast tissues. Collected conceptuses/trophoblasts were snap-frozen in liquid nitrogen and stored at -80 °C until gene and protein expression analyses.

#### *RNA isolation and cDNA synthesis*

Collected tissues were homogenized in 800 µL of FenoZol buffer (A&A Biotechnology, Gdansk, Poland) using Lysing Matrix D beads (MP Biomedicals, Santa Ana, USA) and Fast Prep homogenizer (MP Biomedicals). RNA was isolated from tissues with RNA Mini Kit (A&A Biotechnology), according to the manufacturer's protocol. Integrity and concentration of isolated RNA was analyzed by using Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, USA). Additionally, concentration of RNA was measured with NanoDrop spectrophotometer (Thermo Fisher Scientific, Waltham, USA). To generate cDNA for qPCR reaction total RNA sample (1 µg) was reverse-transcribed with MultiScribe™ Reverse Transcriptase kit (Thermo Fisher Scientific) according to the manufacturer's protocol. cDNA samples were stored in -80 °C for further quantitative PCR (qPCR) analyses.

#### *Quantitative PCR*



Analysis of *PTGFR* gene expression in conceptuses was performed as described previously (Kaczynski & Wacławik 2013). Reverse-transcribed cDNA (3.5 µL) was added to the reaction mixture: 12.5 µl Power SYBR Green master mix (Thermo Fisher Scientific), 2.5 µl of each sense and antisense primer (1 µM; Supplementary Table 1), and 4 µl of nuclease-free water. Specific primers used for real-time RT-PCR are listed in Table 1. The PCR program for *PTGFR* gene was performed as follows: initial denaturation (95 °C, 10 min) followed by 36 cycles of denaturation (95 °C; 15 sec), annealing and elongation (60 °C; 1 min). For actin beta (*ACTB*), cyclophilin A (*PPIA*) and glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) amplification the PCR program was: initial denaturation (95 °C, 10 min) followed by 36 cycles of denaturation (95 °C, 15 sec), annealing (55 °C, 30 sec) and elongation (72 °C 1 min). After PCR, melting curves were acquired by gradual increases in the temperature from 60 to 95 °C to ensure that a single product was amplified in the PCR reaction. All real-time PCR reactions were performed with Applied Biosystems 7900HT Real-Time PCR system (Life Technologies, Carlsbad, USA). Gene expression was estimated using real-time PCR Miner software (Zhao & Fernald 2005). Stability of the reference genes in the porcine conceptuses was assessed using the statistical algorithms Normfinder 2.0 (Andersen *et al.* 2004). Three reference genes were analyzed: *GAPDH*, *PPIA* and *ACTB*. The most stable combination of reference genes was the geometrical mean of *ACTB* and *GAPDH* expression values.

#### *Protein isolation*

Conceptuses (days 10-17)/trophoblasts (days 18-25) collected from pregnant gilts were homogenized on ice in 150 µL of homogenization buffer (50 mM Tris-HCl, pH 8.0; 150 mM NaCl, 1 mM EDTA) supplemented with protease inhibitor cocktail (Sigma-Aldrich, Saint Louis, USA). Homogenates were then centrifuged for 15 min at 800 × g at 8 °C and stored at – 80 °C

for further analysis. The protein concentration was determined with Bradford Assay. PTGFR protein abundance in conceptus homogenates was assessed by Western Blot analysis.

#### *Western Blot*

Western Blot analysis for PTGFR protein expression in conceptuses was performed as described previously (Kaczynski & Wacławik 2013). Briefly, equal amounts of protein samples (40 µg) were separated on 10% SDS PAGE. Proteins were electroblotted onto 0.2 mm PVDF membrane. After blocking in 5% nonfat dry milk, the blots were incubated overnight at 4 °C with primary antibodies (Table 2) and afterwards with 1:20000 dilution of secondary anti-rabbit horseradish peroxidase antibodies (Bio-Rad Laboratories, Hercules, USA) for 90 min at room temperature. Immune complexes were visualized using Clarity Western ECL Substrate (Bio-Rad). Sample loading was standardized to expression of GAPDH. Signal was quantitated using Versa-Doc 4000M imaging system (Bio-Rad Laboratories).

**Experiment 2:** The effect of PGF2 $\alpha$  on global gene expression profile in porcine trophoblast cells

#### *Incubation of the porcine primary trophoblast cells with PGF2 $\alpha$ .*

Porcine trophoblast cells were isolated as described previously (Wacławik *et al.* 2013). Crossbred gilts (n=5) of similar age and genetic background, were inseminated and slaughtered on day 15 of pregnancy at the local abattoir. Conceptuses were recovered from uteri by gentle flushing of each uterine horn with medium M199 (Sigma-Aldrich) containing 0.1% (wt/vol) bovine serum albumin (BSA), penicillin (100 IU/mL, Sigma-Aldrich), and streptomycin (100 µg/mL, Sigma-Aldrich), warmed up to 37°C. Conceptuses were separated from flushing medium by centrifugation for 10 min at 150 × g at 8°C. Trophoblast tissue was dissected from the

embryonic disc region. Trophoblast cells were then non-enzymatically dispersed by pipetting. After dispersion, the cells were washed three times with sterile medium M199 with antibiotics and 0.1% BSA, resuspended in sterile M199 containing antibiotics and 5% newborn calf serum (NCS, Sigma-Aldrich) and seeded on human collagen I-coated 6-well plates (BioCoat™ 356400; BD Biosciences, Bedford, USA). Adherent cells were washed with PBS 48 h after plating to remove contaminating aggregates. Additionally, to assess the purity of cell cultures, isolated cells were stained for the presence of the trophoblast marker - cytokeratin as described previously (Blitek et al., 2012). After reaching 70-80% confluence, the cells were washed with sterile PBS. The following treatments were performed: PGF2 $\alpha$  (100 nM; 1  $\mu$ M; Sigma-Aldrich) and control (medium M199 with vehicle). Treated cells were incubated for 24 h at 37 °C in humidified atmosphere containing 95% air and 5% CO<sub>2</sub>. After incubation, culture media were collected and frozen. Cells were lysed with Fenzol buffer (A&A Biotechnology), harvested and stored at -80°C until isolation of RNA.

#### *Global gene expression profiling by using expression microarrays*

Total RNA was isolated from trophoblast cell lysates as described in experiment 1 and destined for downstream analyses: global gene expression profiling (expression microarray analysis) and qPCR. Microarray analysis was performed starting from 100 ng total RNA isolated from trophoblast cells after *in vitro* experiment (Experiment 2). Cy3-labeled cRNA was produced with the Low-Input Quick Amp Labeling Kit, one-color (Agilent Technologies), and hybridized to the Agilent 4x44k Porcine Gene Expression microarrays (G2519F-026440) according the manufacturer's instructions. Hybridized and washed slides were scanned at 2- $\mu$ m resolution with an Agilent DNA Microarray Scanner (G2505C; Agilent Technologies). Image processing was performed with Feature Extraction Software 10.5.1.1 (Agilent Technologies). Signals were

220 filtered based on “well above background” flags (detection in three of four samples) and  
221 normalized with the BioConductor package VSN (Huber *et al.* 2002). For quality control,  
222 normalized data were analyzed with a distance matrix and a heatmap based on pair-wise  
223 distances (BioConductor package Geneplotter). Differentially expressed genes (DEGs) were  
224 identified in the contrast (pairwise comparison) “PGF2 $\alpha$ -treated cells” vs. “vehicle-treated cells”  
225 using the BioConductor package LIMMA (Linear Model for Microarray Analysis) (Smyth  
226 2004). Low number of genes showing expression differences leads to a too strong correction of  
227 nominal P-values and a very low power to detect true DEGs (Hackstadt & Hess 2009).  
228 Regarding the sensitivity problem of the FDR in case of a low number of DEGs, the cut-off  
229 values were set as follows:  $\geq 1.2$ -fold difference in expression values with a p-value less than  
230 0.05. Significant probes were annotated based on mapping of the probe sequences (60 nt  
231 sequences) to the porcine genome (SusScrofa 11.1). Known and potential human ortholog or  
232 homolog genes were assigned using a custom ortholog annotation database (Mammalian  
233 Ortholog and Annotation Database, MOAdb; JT Bick, SE Ulbrich and S Bauersachs,  
234 unpublished data). If a gene in the list was represented by more than one probe sequence, the  
235 mean fold-change and p-value were calculated. To visualize the distribution of expression  
236 signals of DEGs among samples, hierarchical clustering using Pearson correlation distance was  
237 performed using Multiexperiment Viewer software (MeV) (Saeed *et al.* 2003).

### 238 *Functional annotation of microarray data*

239 Lists of DEGs generated by LIMMA analysis were used as input data for functional annotation.  
240 To study the effect of PGF2 $\alpha$  on the global gene expression profile in trophoblast cells, open-  
241 source and commercial software was applied. The Database for Annotation, Visualization and  
242 Integrated Discovery (DAVID) (Huang *et al.* 2009a, Huang *et al.* 2009b) was used to calculate

the fold enrichment of identified gene ontology (GO) terms using following databases: Functional Categories (UP\_KEYWORDS); gene ontology Biological Process (GOTERM\_BP\_FAT), Cellular Component (GOTERM\_CC\_FAT), Molecular Function (GOTERM\_MF\_FAT); General Annotations (SP\_COMMENT); Pathways (BIOCARTA; KEGG PATHWAY); Protein Domains (INTERPRO) and Protein Interactions (UCSC\_TFBS). Results generated by DAVID were summarized in tabular format. Topp Cluster software (Kaimal *et al.* 2010) was used to identify gene ontologies enriched by DEGs and to generate a network showing the shared and list-specific functional features. Results were summarized in tabular format and visualized by interaction network. To identify signaling pathways, molecular networks, and biological functions for DEGs Ingenuity Pathway Analysis (IPA; v. 01.12; Qiagen, Redwood City, USA) were used. Results were summarized in tabular and in graphic formats.

#### *Validation of microarray results*

To verify results obtained in microarray analysis we validated the expression of *ADAM9*, *AGER*, *AMBP*, *BMP2*, *DECRI*, *IL1A*, *KNG1*, *LPAR1*, *MASPI*, *MFGE8*, *MMP2*, *PROX1*, *S100G*, *SLCO2A1*, *STC2*, *THBS1*, *TLR3* and *VTN* genes using real-time RT-PCR method. Additionally, based on our previous studies (Kaczynski *et al.* 2016) and literature data we studied whether PGF2 $\alpha$  affected the expression of *BGN*, *IL6*, *IL6R*, *MMP9*, *TGFB3*, *TIMP1* and *TIMP2* genes. Based on microarray results, we also decided to evaluate the gene expression profile of *MMP9* in porcine conceptuses (days 10-17)/ trophoblasts (days 18-25) throughout pregnancy development. cDNA was generated from RNA isolated from trophoblast cells as described in Experiment 1. Real-time RT-PCR was performed using TaqMan assays (Thermo Fisher Scientific; Table 1) accordingly to the manufacturer's protocol. Results from qPCR were analyzed as described in

266 Experiment 1. Stability of the reference genes in the porcine trophoblast cells was assessed using  
267 the statistical algorithm Normfinder 2.0 (Andersen *et al.* 2004). Three reference genes were  
268 analyzed: *GAPDH*, *PPIA* and *ACTB*. The most stable combination of reference genes was the  
269 geometrical mean of *ACTB* and *GAPDH* expression values.

270 **Experiment 3:** The effect of PGF2 $\alpha$  on trophoblast cell adhesion and proliferation.

271 Porcine primary trophoblast cells were isolated as described previously (Waclawik *et al.* 2013)  
272 with some modifications. Briefly, recovered conceptuses were washed three times with medium  
273 M199 supplemented with 5% (v/v) NCS and 0.1% (m/v) BSA. Subsequently, trophoblast tissue  
274 underwent mild digestion in 0.25% trypsin solution (Biomed, Lublin, Poland) for 30 min at  
275 37°C. After digestion, solution was neutralized with M199 supplemented with 10% (v/v) NCS.  
276 Cells were then centrifuged at 150  $\times$  g for 10 min and washed three times with medium M199  
277 supplemented with 5% (v/v) NCS. After washing the cells were re-suspended in medium M199  
278 with 1% (v/v) NCS. Viability and cell number was assessed with trypan blue dying.

279 For adhesion assay, cells ( $1 \times 10^6$  cells/mL) were pre-incubated with medium M199 containing  
280 vehicle (0.01% ethanol) or PGF2 $\alpha$  (100 nM, 1  $\mu$ M) with/without 50  $\mu$ M of PTGFR antagonist  
281 (AL8810, Sigma Aldrich) for 30 min at 37°C. Subsequently, 100  $\mu$ L of each cell suspension was  
282 transferred onto Millicore Cell Adhesion Strips coated with human fibronectin (ECM101;  
283 Millipore, Billerica, USA) and incubated for 3 h at 37°C. All treatments were performed in  
284 triplicates. After incubation, cell adhesion was measured using colorimetric method accordingly  
285 to the manufacturer's protocol.

286 Cells used in proliferation assay were re-suspended in culture medium (M199 supplemented with  
287 5% NCS) in concentration  $5 \times 10^4$  cells/mL. After attachment, the cells were incubated for 48 h

at 37°C in humidified atmosphere (95% air, 5% CO<sub>2</sub>) with medium M199 containing vehicle (0.01% ethanol) or PGF2 $\alpha$  (100 nM, 1  $\mu$ M) or stable PGF2 $\alpha$  analogue (fluprostenol; 100 nM, 1  $\mu$ M) with/without 50  $\mu$ M of PTGFR antagonist (AL8810). Based on our previous results (Kaczynski *et al.* 2016), 20% NCS was used as a positive control. After 48 h of treatment, proliferation was determined using the Cell Titer 96 Aqueous One Solution Proliferation Reagent (Promega) according to the manufacturer's instructions. Experiments were repeated 6 times in triplicates. Fold difference was determined by dividing the absorbance obtained by PGF2 $\alpha$ -treated cells (with/without inhibitors) by the absorbance obtained by vehicle-treated cells.

**Experiment 4:** Effect of PGF2 $\alpha$  on downstream targets potentially involved in porcine trophoblast cells adhesion and proliferation.

To determine the protein expression of downstream targets of PGF2 $\alpha$  involved in porcine trophoblast cells adhesion and proliferation, we used previously described (Waclawik *et al.* 2013) *in vitro* model in which primary trophoblast cells were incubated for 24 h with either vehicle (0.01% ethanol) or PGF2 $\alpha$  (100 nM, 1  $\mu$ M) in the presence/absence of 50  $\mu$ M AL8810. After incubation cells were lysed with RIPA buffer (PBS; pH 7.4; 1% Triton X-100; 0.5% sodium deoxycholate; 0.1% sodium dodecyl sulfate; 1 mM EDTA) containing Protease Inhibitor Cocktail (Sigma-Aldrich) and Phosphatase Inhibitor Cocktail 2 (Sigma-Aldrich). Content of MAPK1/3, pMAPK1/3, FAK and pFAK in cell homogenates was determined using Western blot and was normalized against GAPDH expression. Phosphorylation of MAPK and FAK protein was calculated by dividing the relative content of phosphorylated to non-phosphorylated protein.

*Western Blot*

309 MAPK1/3 and FAK protein phosphorylation was evaluated using Western Blot analysis as  
310 described previously (Waclawik *et al.* 2013). Briefly, equal amounts of protein samples (18 µg)  
311 from conceptus cell lysates were separated on 10% SDS PAGE. Proteins were electroblotted  
312 onto 0.2 mm PVDF membrane. After blocking in 5% bovine serum albumin blots were  
313 incubated overnight at 4 °C with primary antibodies (Table 2) and afterwards with 1 : 20 000  
314 dilution of secondary anti-rabbit horseradish peroxidase antibodies (Bio-Rad Laboratories) for 90  
315 min at room temperature. Immune complexes were visualized using Clarity Western ECL  
316 Substrate (Bio-Rad). Sample loading was standardized to expression of GAPDH. Signal was  
317 quantitated using Versa-Doc 4000M imaging system (Bio-Rad Laboratories).

#### 318 *Statistical analyses*

319 Results from *in vitro* experiments (cell adhesion and proliferation assays), Western Blot and  
320 qPCR studies were analyzed by one-way ANOVA followed by Tukey's test. All statistical  
321 analyses were conducted using GraphPad PRISM v. 6.01 software (GraphPad Software Inc., San  
322 Diego, USA).

## 323 **RESULTS**

324 **Experiment 1:** Expression of PTGFR gene and protein increases in the conceptus/trophoblast  
325 during the implantation period.

326 Expression of PTGFR mRNA was elevated in conceptuses/trophoblasts from day 14 until day 19  
327 of pregnancy (the implantation period;  $p < 0.05$ ) compared with conceptuses/trophoblasts on days  
328 10-12 (the preimplantation period). The highest expression of PTGFR mRNA was observed in  
329 conceptuses/trophoblasts from days 16-19 of pregnancy (Fig. 1A) and was 48-fold greater than  
330 in conceptuses/trophoblasts from days 10-12 of pregnancy ( $p < 0.05$ ). PTGFR protein expression



was elevated at the implantation period (days 14-15, 16-19 of pregnancy) when compared to later stage (days 20-25 of pregnancy;  $p < 0.05$ ; Fig. 1B). Expression of PTGFR protein in day 10-12 conceptuses was not evaluated due to insufficient amount of material for both gene and protein analyses. Thus, in collected material only expression of PTGFR gene was possible to analyze.

**Experiment 2:** Effect of  $\text{PGF2}\alpha$  on global gene expression profile in porcine trophoblast cells.

#### *Characterization of trophoblast cells*

The purity of the isolated cells was assessed by the evaluation of the presence of the trophoblast marker - cytokeratin and cell morphology. Isolated trophoblast cells presented uninuclear morphology (Suppl. Fig. 1A). Positive immunoreaction for cytokeratin confirmed the epithelial phenotype of trophoblast cells (Suppl. Fig. 1B). Antiserum-specific isotype control (negative control) used at the same dilution and protein concentration as the primary antibody is shown in Supplemental Figure 1B (lower-left panel). Purity of cell cultures was assessed at 98%.

#### *Global gene expression profiling by using expression microarrays*

The porcine trophoblast cells' response towards the  $\text{PGF2}\alpha$  treatment was characterized using a porcine Agilent microarray assay. Differential gene expression between the two experimental groups ("PGF2 $\alpha$ -treated cells" vs. "vehicle-treated cells") was evaluated. The number of detected probes passing the filters was 27045. Pairwise distance analysis based on all detectable probes revealed grouping replicates, but differences between PGF2 $\alpha$ -treated and vehicle-treated samples are also indicated in the heat map (Suppl. Fig. 2). Using LIMMA package, 810 probes were found as differentially regulated (fold change  $< / > 1.2$ ;  $p < 0.05$ ; Suppl. Table 1). Annotation of probe sequences revealed 576 DEGs (216 down-regulated, 360 up-regulated) affected by PGF2 $\alpha$ .

The five DEGs showing highest upregulation in the pairwise comparison “PGF2 $\alpha$ -treated cells” vs. “vehicle-treated cells” were obtained for the following genes: *SI00G* (3.9-fold), *NPEPPS* (2.6-fold), *PDE1B* (2.5-fold), *KNGL1* (2.3-fold), *AMBP* (2.0-fold), whereas the five most downregulated genes (suppressed by PGF2 $\alpha$ ) were: *SELENBP1* (-1.8-fold), *DIO1* (-1.8-fold), *ENTPD8* (-1.8-fold), *LYZ* (-1.7-fold), *FMO1* (-1.6-fold). Hierarchical clustering of the obtained DEGs based on Pearson correlation revealed treatment grouping of analyzed samples with two main distinct clusters of genes with uniform distribution of expression signals (Fig. 2).

*Functional annotation of microarray data*

Functional terms enriched for up- and down-regulated DEGs from both experimental groups were identified by DAVID analysis. For up-regulated DEGs, DAVID identified 83 functional annotation clusters with enrichment scores from 1.04 up to 3.96 (Suppl. Table 2), whereas for down-regulated DEGs 62 functional annotation clusters were identified with enrichment scores from 1.06 up to 6.79 (Suppl. Table 3). The most interesting functional terms of overrepresented annotation clusters enriched for up-regulated genes were related to focal adhesion, cell migration, hypoxia, response to fibroblast growth factor (FGF2) and transforming growth factor beta (TGFB), and regulation of cell proliferation and MAPK cascade (Table 3). Terms overrepresented by down-regulated genes were mainly related to fatty acid biosynthetic process, cell migration, anion transport, response to interferon gamma, and placenta development (Table 3). Complete results from Functional Annotation Clustering were summarized in Supplementary Tables 2 and 3.

Using ToppCluster software, GO terms (biological process, cellular component and molecular function) and pathways (KEGG) enriched by DEGs were identified and summarized in tabular format (Suppl. Table 4). Similarly, as in DAVID analysis, overrepresented terms were related to

processes potentially important for embryo implantation and development of early pregnancy such as: adhesion, immune response, placenta development, morphogenesis, cytoskeleton organization and others. The most interesting enriched terms from PGF2 $\alpha$ -up-regulated and PGF2 $\alpha$ -down-regulated clusters were visualized as a network (Fig. 3).

Using Ingenuity Pathway Analysis on 577 DEGs, the most interesting over-represented canonical pathways were associated with regulation of lipid metabolism, inflammation, and cholesterol catabolism (LXR/RXR;  $p=3.47E-06$ ), as well as with integrin ( $p=2.2E-04$ ) and mTOR ( $p=1.701E-02$ ) signaling (Suppl. Table 5). The main functional terms derived from IPA analysis showed similar results, compared to DAVID analysis, with highly involved functional terms such as embryonic development, inflammatory response, cellular growth and proliferation and lipid metabolism. (Suppl. Fig. 3; Suppl. Table 6). Upstream analysis revealed that identified DEGs can be also regulated by other factors than PGF2 $\alpha$  factors (Suppl. Table 7). The most interesting factors potentially stimulating DEGs were estradiol-17 $\beta$ , HOXA10 and TGFB1 and 2.

### *Effect of PGF2 $\alpha$ on the selected gene expression in porcine conceptuses.*

Validation of microarray results using qPCR confirmed expression of 14 out of 18 selected genes (*IL1A*, *MFGE8*, *MMP2*, *SLCO2A1*, *STC2*, *ADAM9*, *AGER*, *AMBP*, *BMP2*, *LPAR1*, *MASPI*, *S100G*, *THBS1* and *VTN*), whereas 4 of them (*KNG1*, *PROX1*, *DECRI* and *TLR3*) showed diverse expression in the qPCR to that detected by microarray analysis (Suppl. Table. 8). Results from qPCR revealed that PGF2 $\alpha$  (100 nM) acting on trophoblast cells stimulated expression of *ADAM9*, *VTN*, *LPAR1*, *BMP2*, *DECRI* and *THBS1* genes ( $p<0.05$ ). Treatment of the trophoblast cells with 1  $\mu$ M of PGF2 $\alpha$  resulted in increased expression of *AGER*, *AMBP*, *BGN*, *IL6R*, *S100G*, *TLR3* and *MASPI* genes ( $p<0.05$ ) and in down-regulation of *MFGE8*, *SLCO2A1*, *TIMP1*, *TIMP2*, *KNG1*, *MMP9*, *SCT2* and *TGFB3* gene expression ( $p<0.05$ ). Expression of *IL1A*, *MMP2*

399 and *PROX1* genes was decreased in the trophoblast cells treated with both doses (100 nM; 1  $\mu$ M)  
400 of PGF2 $\alpha$  ( $p < 0.05$ ). Results from qPCR analyses are shown in the Figure 4. Additionally, we  
401 evaluated the expression profile of *MMP9* in conceptuses (days 10-17) / trophoblasts (days 18-  
402 25) at different stages of development. We found that the abundance of *MMP9* mRNA was  
403 lowest at the period corresponding to maternal recognition of pregnancy (days 10-12 of  
404 pregnancy) and at the beginning of implantation (days 14-15). Expression of *MMP9* was  
405 intermediate during implantation (days 16-19 of pregnancy) and markedly increased during  
406 placenta development (days 20-25 of pregnancy;  $p < 0.05$ ; Fig. 4E).

407 **Experiment 3:** PGF2 $\alpha$  stimulates adhesion and proliferation of the porcine trophoblast cells.

408 We demonstrated that PGF2 $\alpha$  (100 nM; 1  $\mu$ M) acting through its receptor increased adhesion of  
409 trophoblast cells to fibronectin ( $p < 0.05$ ; Fig. 5A). Stimulating effect of PGF2 $\alpha$  (100 nM and 1  
410  $\mu$ M) was blocked by using PTGFR antagonist (AL8810). AL8810 used alone did not have any  
411 effect on cell adhesion.

412 During early pregnancy in mammals, rapid transformation of conceptus morphology and  
413 conceptus cell differentiation should be accompanied by increased cell proliferation. In the  
414 present study, we evaluated the influence of PGF2 $\alpha$  on conceptus cell proliferation during  
415 implantation period. We found that PGF2 $\alpha$  (100 nM) as well as its stable analog – fluprostenol  
416 (100 nM), acting through PTGFR stimulated proliferation of porcine trophoblast cells ( $p < 0.05$ ;  
417 Fig. 5B). The effects of PGF2 $\alpha$  (100 nM) and fluprostenol (100 nM) were abolished by using  
418 AL8810. AL8810 used alone had effect similar to the control.

419 **Experiment 4:** PGF2 $\alpha$  acting on trophoblast cells increases phosphorylation of factors  
420 potentially involved in adhesion and proliferation processes.

Since we previously indicated involvement of FAK and MAPK (Waclawik *et al.* 2013) in adhesion of trophoblast cells and as MAPK signaling is also involved in cell proliferation we determined whether PGF2 $\alpha$  may stimulate phosphorylation of these proteins in the trophoblast cells. In the present study, we demonstrated for the first time that PGF2 $\alpha$  stimulated phosphorylation of MAPK1/3 (Fig. 5C) and FAK (Fig. 5D) proteins ( $p < 0.05$ ) in porcine trophoblast cells and that these effects were mediated through PGF2 $\alpha$  receptor (Fig. 5C and D).

## DISCUSSION

In the present study, we demonstrated for the first time the para- and/or autocrine mechanisms of prostaglandin F2 $\alpha$  action on conceptus/trophoblast cells during the implantation period. We also described the expression profile of PGF2 $\alpha$  receptor (PTGFR) in porcine conceptuses at different stages of their development.

Results from our experiments discussed below provide a new perspective on the role of PGF2 $\alpha$  in embryo-maternal communication in the pig. We postulate that PGF2 $\alpha$ , which is highly abundant in the uterine lumen during early pregnancy, is not an undesirable factor but instead is an important hormone supporting processes related to proper embryo development and implantation. In the present study, we examined, for the first time, the expression profiles of PTGFR mRNA and protein in porcine conceptuses/trophoblasts during early pregnancy. Maximal expression of the PTGFR gene in conceptuses/trophoblasts occurred during the implantation period. Similarly, increased abundance of PTGFR protein was observed on days 14-19 of pregnancy. These results concur with our previous findings that PGF2 $\alpha$  synthase protein expression is increased in conceptuses/trophoblasts from days 14 to 25 compared to days 10-12 of pregnancy (Waclawik & Ziecik 2007). Strong signals of PTGFR protein expression are observed in the ovine trophectoderm on days 16, 18 and 20 of pregnancy (Dorniak *et al.* 2011).

PGs secreted together with IFNT by ovine conceptuses regulate endometrial gene expression and functions that are important for conceptus growth and development (Dorniak *et al.* 2012). Our results are also consistent with transcriptomic data, in which expression of the PTGFR gene in day 14 filamentous conceptuses was 14-fold greater than in day 10 (spherical) -12 (filamentous) conceptuses (Ross *et al.* 2009). Interestingly, we indicated the up-regulation of endometrial PTGFR protein during the implantation period (Kaczynski & Wacławik 2013). These results strongly support the hypothesis that PGF2 $\alpha$  secreted by the endometrium and conceptuses into the uterine lumen can act on trophoblasts in an auto- and/or paracrine manner.

In the present study, we evaluated the effect of PGF2 $\alpha$  on global gene expression profiles in porcine conceptuses at the onset of the implantation period. Using different bioinformatics software, we were able to demonstrate that PGF2 $\alpha$  potentially affects a broad range of processes and functions related mainly with focal adhesion, extracellular matrix binding, cytoskeleton organization, cell migration and proliferation, but also with immune processes, metabolism, response to hypoxia, growth factor signaling and ion homeostasis. Intriguingly, similar processes (e.g., protein kinase regulator activity, cell motility, transport) identified in conceptuses undergoing the transition from day 12 to day 14 filamentous forms (Ross *et al.* 2009) were also observed in trophoblast cells treated with PGF2 $\alpha$ . Moreover, it is interesting that analysis of potential up-stream regulators of genes which were differentially regulated by PGF2 $\alpha$  revealed that these DEGs may be also regulated by other factors such as estradiol-17 $\beta$ , HOXA10 or TGFB which are important players in the embryo-maternal dialogue during early pregnancy (reviewed in Wacławik *et al.* 2017).

Due to the relatively low fold change threshold for detection of DEGs it is recommended to validate these results for corresponding DEGs if more in-depth studies are projected based on our

transcriptomic analyses results. In the present study, we validated part of the microarray results using qPCR and functional in vitro experiments. Validation of expression of particular genes of interest (*AGER*, *AMBP*, *MASP1*, *MFGE8*, *PROX1*, *SLCO2A1*, *VTN*, *ADAM9*, *LPAR1*, *BMP2*, *DECRI1*, *THBS*, *S100G*, *STC2*, *IL1A* and *TLR3*) confirmed overall the results from the microarray analyses. Additionally, we analyzed the PGF2 $\alpha$ -mediated expression of genes that are potentially important in embryo-maternal interactions during the implantation period (*BGN*, *MMP2*, *MMP9*, *TIMP1*, *TIMP2*, *KNG1*, *TGFB3*, *IL6*, *IL6R* and *TGFB3*). Results of the microarray and qPCR analyses revealed that the PGF2 $\alpha$  affected the expression of genes related to processes crucial for successful implantation, such as: ECM organization, ECM protein binding, focal adhesion, inflammatory response, cell proliferation, migration and motility or activation of intracellular protein kinases. Here, we briefly discuss the importance of validated genes in the most important processes accompanying the implantation process.

In all mammalian species, during the peri-implantation period formation of the placenta is preceded by adhesion of trophoblast cells to luminal epithelium of the endometrium (Geisert *et al.* 2015). This requires a profound rearrangement of endometrial tissue that is essential for successful implantation of embryos. Reorganization of tissue structures is related to processes such as ECM remodeling and vasculature development and is tightly controlled by a number of factors. Metalloproteinases are factors regulating ECM remodeling. MMPs together with their associated inhibitors (TIMPs) act concomitantly regulating aspects of reproductive function (reviewed in Curry & Osteen 2003). MMP2 and MMP9 were reported to mediate human trophoblast cell invasion into matrigel *in vitro* (Bischof *et al.* 1995). Recently, we reported PGF2 $\alpha$ -stimulated expression of the MMP9 gene in porcine endometrium, suggesting its involvement in ECM remodeling (Kaczynski *et al.* 2016). In this study, we observed a decrease

490 in *MMP2* and *MMP9* mRNA content in porcine trophoblast cells in response to  $\text{PGF2}\alpha$   
491 treatment. Simultaneously, we noticed that  $\text{PGF2}\alpha$  up-regulated expression of the *TIMP2* gene  
492 which is an inhibitor of *MMP2* and *MMP9*. These results correspond to the *MMP9* gene  
493 expression profile in porcine conceptuses at different stages of development that was evaluated  
494 in the present study. Intriguingly, we found that  $\text{PGF2}\alpha$  acting on human trophoblast cells has an  
495 opposite effect, i.e. it increases *MMP9* gene expression that is probably related to invasive type  
496 of implantation of human trophoblast (Baryla *et al.* 2017). We suggest that the down-regulation  
497 of *MMP2* and *9* and up-regulation of *TIMP2* mRNA expression in porcine conceptuses could be  
498 an effect of action of endometrium which by secreting  $\text{PGF2}\alpha$  may protect the endometrial tissue  
499 against excessive degradation of its ECM and this may be related to the non-invasive type of  
500 implantation specific for the pig. Moreover, we demonstrated that  $\text{PGF2}\alpha$  differentially  
501 regulated other genes (*BGN*, *THBS*, *VTN*, *MFGE8*, *ADAM9*, *KNG1*, *AMBP* and *PROX1*) that  
502 were reported to be involved in ECM remodeling, cell adhesion and proliferation in different  
503 mammalian species (Kaczynski *et al.* 2016, Bowen *et al.* 1996, Couchman *et al.* 1990,  
504 Kolakowska *et al.* 2017, Bloor *et al.* 2002, Taylor *et al.* 1997, Barua *et al.* 2017, Kim *et al.* 2006,  
505 Vonnahme *et al.* 2004, Hettinger *et al.* 2001, Kim *et al.* 2013). Results from functional *in vitro*  
506 experiments performed herein confirmed results from gene expression studies and support the  
507 conclusion that  $\text{PGF2}\alpha$  acting through its receptor in trophoblast cells stimulates adhesion of  
508 trophoblast cells to ECM proteins. Interestingly, we recently demonstrated that the role of  $\text{PGE2}$   
509 in increasing trophoblast adhesion is not species-specific because the mechanism is  $\text{PTGER2}$ -  
510 and integrin-dependent in both porcine and human trophoblast cells (Waclawik *et al.* 2013).  
511 Moreover, iloprost (prostacyclin analogue) acting through prostacyclin membrane receptors  
512 ( $\text{PTGIR}$ ) stimulated porcine day 14 trophoblast cells to adhere to fibronectin (Morawska-



Pucinska *et al.* 2014). Thus, the present report emphasizes the role of prostaglandins in proper control of the adhesion cascade during the implantation period in the pig.

During the peri-implantation period, porcine conceptuses undergo rapid transformation. On day 12 of pregnancy, trophoblasts elongate to more than 100 millimeters in length (Anderson, 1978, Geisert *et al.* 1982). It has been stated that the conceptus elongation process is more dependent on cell outgrowth than cell division (Perry, 1981). However, elongation is not the only process occurring during conceptus development. Cellular differentiation is also very important for embryonic development in all mammalian species. This process requires tight control over cell proliferation, migration and cell-cell interaction. The potential role of TGFB, LPA1, PROX1, AMBP and BMP2 in pregnancy establishment was reported in a number of mammals (Kim *et al.* 2013, Blitek *et al.* 2013, Jeong *et al.* 2016, McKeehan *et al.* 1986, Lee *et al.* 2007). Interestingly, IL6 which is mostly related to immunological processes has been reported to stimulate trophoblast cell proliferation and promote their adhesion to fibronectin (Blitek *et al.* 2012). In the present study, we found that PGF2 $\alpha$  did not affect *IL6* mRNA, however, it increased IL6 receptor (*IL6R*) mRNA content in porcine day 15 trophoblast cells. The present study is the first demonstrating the role of PGF2 $\alpha$  in promoting trophoblast cell proliferation in any mammalian species. We recently reported an indirect influence of PGF2 $\alpha$  on uterine endothelial cell proliferation (Kaczynski *et al.* 2016). Moreover, fluprostenol (PGF2 $\alpha$  analogue) was reported to stimulate the expression of proteins related to proliferation of bovine endometrial cells (Zhang *et al.* 2017).

During the implantation period in some mammals, including pigs both pro- and antiinflammatory processes are activated at the embryo-maternal interface and the proper balance between these two kinds of immunological responses is crucial for successful development of pregnancy

(reviewed in Waclawik 2011). In the present study, we found that  $\text{PGF2}\alpha$  differentially regulated the expression of *KN1*, *MFG8*, *AMBP*, *IL1*, *IL6R*, *MAS1*, *AGER* and *TLR3* genes that are involved in modulation of immunological processes in many species (Vonnahme *et al.* 1999, Allen *et al.* 2002, Tan *et al.* 2015, Tuo *et al.* 1996, Prins *et al.* 2012, Wang *et al.* 2007, Bebraum *et al.* 2008, Zhang *et al.* 2007). Thus, we infer that  $\text{PGF2}\alpha$  by differentially regulating genes in trophoblast cells may contribute to the control of immune interactions between developing conceptuses and the endometrium.

The importance and function of calcium during early embryo development and implantation have been well studied (reviewed in Whitaker 2006). Binding endometrial epithelial cells to trophoblast cells results in calcium influx in endometrial epithelial cells in humans (Tinel *et al.* 2000). In the porcine uterine lumen, concentration of calcium ions increases during the peri-implantation period (Geisert *et al.* 1982). Bikunin, one of the products of the *AMBP* gene, has been reported to inhibit the release of intracellular calcium ions induced by lipopolysaccharide (Kanayama *et al.* 1995). Stanniocalcin (STC), a glycoprotein regulating calcium homeostasis and has been suggested to be a luminal epithelial marker for implantation in pigs (Song *et al.* 2009). Another factor related to calcium ion homeostasis in endometrium during pregnancy is S100G protein also known as calbindin-d9k (Choi *et al.* 2009). Our data indicate that  $\text{PGF2}\alpha$  by regulating *AMBP*, *STC2* and *S100G* gene expression in porcine conceptuses may be an upstream regulator of factors involved in calcium homeostasis. Our data suggest that in porcine conceptuses  $\text{PGF2}\alpha$  regulates *MFG8* and *DEC1* which are involved in fatty acid metabolism, fatty-acid resorption and placental transport (Khalifeh-Soltani *et al.*, 2013; Kunau *et al.*, 1978, Marques *et al.*, 2009).

Prostaglandin signaling is crucial for proper conceptus development (Dorniak *et al.* 2011, Kennedy *et al.* 2007). *SLCO2A1* was suggested to play a critical role in supporting the establishment and maintenance of pregnancy by regulating PG transport at the maternal–fetal interface in pigs. Expression of *SLCO2A1* mRNA in day 15 conceptuses is decreased compared to day 12 conceptuses (Seo *et al.* 2014). Accordingly, we found down-regulation of *SLCO2A1* gene expression in porcine trophoblast cells in response to PGF2 $\alpha$  treatment. This may suggest that PGF2 $\alpha$  by regulating its own transporter expression in trophoblast cells may autoregulate its secretion by conceptuses during implantation period.

Processes accompanying the implantation process such as cell adhesion and proliferation are triggered by activation of particular intracellular signaling pathways. Results from gene expression studies indicated that PGF2 $\alpha$  enriched terms related to activation of protein kinases, such as MAP kinase activity and protein phosphorylation. In the present study, we demonstrated that PGF2 $\alpha$  stimulated MAPK1/3 and focal adhesion kinase (FAK) protein phosphorylation in trophoblast cells. Interestingly, PGF2 $\alpha$  has been reported to stimulate tyrosine phosphorylation of p125 FAK in NIH-3T3 cells (Watanabe *et al.* 1994) and in 293-EBNA cells stably expressing isoform A of the PTGFR prostanoid receptor (Pierce *et al.* 1999). PTGFR is a G-protein-coupled receptor activating Gq11 protein (Bos *et al.* 2004) and it has been demonstrated that genes up-regulated at the end of gestation in a Gq/11-dependent manner in ovarian (granulosa/luteal) cells included genes involved in focal adhesion and extracellular matrix interactions (Waite *et al.* 2016). Moreover, in human adenocarcinoma cells (Ishikawa cell line), PGF2 $\alpha$  was able to induce MAPK1/3 phosphorylation (Sales *et al.* 2005). We also found that PGE2 induced phosphorylation of MAPK1/3 and FAK. Taking all the above facts together, we speculate that PGF2 $\alpha$  acting through its receptor in trophoblast cells may activate Gq11 protein that leads to

581 increased MAPK1/3 and FAK phosphorylation. This may result in enhanced adhesion of porcine  
582 trophoblast cells to ECM proteins.

583 In summary, the present study indicates a new role for PGF2 $\alpha$  secreted both by the conceptuses  
584 and endometrium during the implantation period in pigs. Results from global gene expression  
585 profiling indicate that PGF2 $\alpha$  acting in an auto- and/or paracrine manner is involved in processes  
586 important for conceptus development and attachment to the uterine epithelium (cell proliferation  
587 and focal adhesion, extracellular matrix binding, cell migration, cytoskeleton organization,  
588 immune interactions, ion homeostasis, metabolism, activation of TGFB and FGF signaling  
589 pathways, response to hypoxia). Functional *in vitro* experiments confirmed insights from  
590 transcriptomic studies, allowing us to conclude that PGF2 $\alpha$  by inducing transcriptomic changes  
591 in porcine trophoblast cells affects a broad range of processes potentially involved in  
592 implantation and development of the placenta, particularly activation of intracellular protein  
593 kinases (MAPK, FAK) and stimulation of trophoblast cell adhesion and proliferation.

#### 594 **DECLARATION OF INTERESTS**

595 Authors of the manuscript declare that there is no conflict of interest that could be perceived as  
596 prejudicing the impartiality of the research reported.

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- 832



## FIGURE LEGENDS

**Figure 1.** Expression of PTGFR mRNA (A) and protein (B) in the porcine conceptuses/trophoblasts at different stages of development. The representative samples of Western blots are shown in the upper panels. Data are represented as the mean  $\pm$  SEM. Bars with different letter differ significantly ( $p < 0.05$ ).

**Figure 2.** Heatmap showing microarray analysis of DEGs in PGF2 $\alpha$ -treated porcine trophoblast cells (PGF2 $\alpha$  1-4), and corresponding vehicle-treated controls (Control 1-4). Normalized expression data was clustered based on pair wise Pearson correlation using identified DEGs (red: correlation=1; blue: correlation= -1). 576 genes were differentially expressed between the two groups. A total of 360 genes were up-regulated and 216 genes were down-regulated ( $p < 0.05$ ). The full list of DEGs is provided in Supplementary Table 1.

**Figure 3.** Functional map showing shared and treatment-specific functional annotation terms generated in multi-cluster gene functional enrichment analysis for DEGs identified in porcine primary trophoblast cells treated with PGF2 $\alpha$  or vehicle (control). Analysis was performed in ToppCluster software, functional map was edited and adjusted using Cytoscape. The redundant and non-informative terms were removed. Complete results are presented in tabular format in Supplementary Table 4.

**Figure 4.** Expression of selected target genes determined by quantitative (real-time) RT-PCR in porcine primary trophoblast cells treated with PGF2 $\alpha$  (100 nM, 1  $\mu$ M) or vehicle (control). (A-D, F-Y). *TIMP1*-metallopeptidase inhibitor 1, *TIMP2*-metallopeptidase inhibitor 2, *MMP2*-matrix metallopeptidase 2, *MMP9*-matrix metallopeptidase 9, *BGN*-biglycan, *THBS1*-thrombospondin 1, *VTN*-vitronectin, *ADAM9*-ADAM metallopeptidase domain 9, *MFGE8*-milk fat globule-EGF

855 factor 8 protein, *PROX1*-prospero homeobox 1, *TGFB3*-transforming growth factor beta 3,  
 856 *LPAR1*-lysophosphatidic acid receptor 1, *AMBP*-alpha-1-microglobulin/bikunin precursor,  
 857 *BMP2*-bone morphogenetic protein 2, *IL1A*-interleukin 1 alpha, *IL6R*-interleukin 6 receptor,  
 858 *MASP1*-mannan binding lectin serine peptidase 1, *AGER*-advanced glycosylation end-product  
 859 specific receptor, *TLR3*-toll-like receptor 3, *STC2*-stanniocalcin 2, *S100G*-S100 calcium binding  
 860 protein G, *DECRI*-2,4-dienoyl-CoA reductase 1, *SLCO2A1*-solute carrier organic anion  
 861 transporter family member 2A1. Expression of *MMP9* mRNA in the porcine conceptuses/  
 862 trophoblasts at different stages of development (E). Data on panels A-D and F-Y are presented as  
 863 means  $\pm$  SEM of fold change versus control (vehicle). Data on panel E is presented as mean  $\pm$   
 864 SEM. Bars with different letter differ significantly ( $p < 0.05$ ).

865 **Figure 5.** PGF2 $\alpha$  increased adhesion to extracellular matrix protein - fibronectin (A) and  
 866 proliferation (B) of primary porcine trophoblast cells. Effect of PGF2 $\alpha$  on MAPK1/3 (C) and  
 867 FAK (D) phosphorylation in porcine primary trophoblast cells *in vitro*. NCS-newborn calf serum  
 868 (used as a positive control), FLP – fluprostenol (stable prostaglandin F2 $\alpha$  analogue), AL8810 –  
 869 PTGFR antagonist. Data are presented as means  $\pm$  SEM of fold change versus control (vehicle).  
 870 Different letters (a-c) indicate statistically significant differences ( $p < 0.05$ ).

## 871 SUPPLEMENTARY DATA LEGENDS

872 **Supplementary Figure 1** Light microscopy with phase contrast (A) and immunofluorescent  
 873 staining for cytokeratin presence (B) in trophoblast cells isolated from day 15 conceptuses.  
 874 Negative control (mouse IgG) is shown in lower-left part of the figure. Arrows indicate signals  
 875 for cytokeratin.

876 **Supplementary Figure 2.** Gene expression distance matrix of analyzed samples generated in  
 877 Geneplotter library. VSN-normalized microarray expression data was clustered based on pair  
 878 wise correlation using all detectable probes. PGF2 $\alpha$ \_1-4 – porcine trophoblast cells treated with  
 879 PGF2 $\alpha$  (1  $\mu$ M), isolated from gilts 1-4. Control\_1-4 – porcine trophoblast cells treated with  
 880 vehicle (0.01% ethanol) isolated from gilts 1-4.

881 **Supplementary Figure 3.** Selected functional terms overrepresented by DEGs identified by IPA  
 882 analysis determined basing on the identified canonical pathways. Complete results from IPA  
 883 analyses are presented in tabular format in Supplementary Tables 5-7.

884 **Supplementary Table 1.** Results of statistical analysis of microarray data (paired LIMMA).

885 **Supplementary Table 2.** DAVID functional annotation clustering results for up-regulated genes  
 886 in PGF2 $\alpha$ -treated conceptus cells compared to vehicle-treated conceptus cells.

887 **Supplementary Table 3.** DAVID functional annotation clustering results for down-regulated  
 888 genes in PGF2 $\alpha$ -treated conceptus cells compared to vehicle-treated conceptus cells.

889 **Supplementary Table 4.** Enriched GO terms and pathways by up-regulated genes in PGF2 $\alpha$ -  
 890 treated conceptus cells compared to vehicle-treated conceptus cells.

891 **Supplementary Table 5.** Canonical pathways potentially regulated by identified DEGs.

892 **Supplementary Table 6.** Functions affected by identified DEGs.

893 **Supplementary Table 7** Upstream regulators affecting expression of identified DEGs.

894 **Supplementary Table 8.** Comparison of results from qPCR and microarray gene expression  
 895 analyses.

896

FIGURE 1

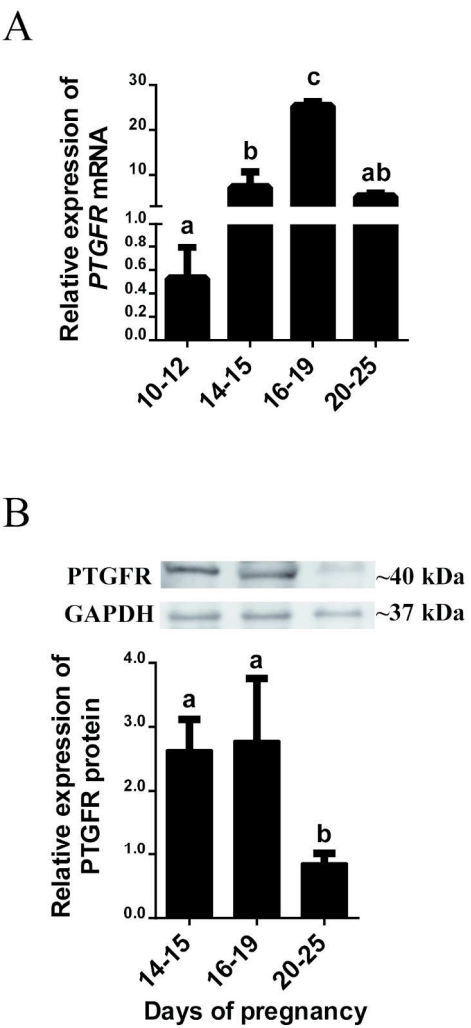


Figure 1. Expression of PTGFR mRNA (A) and protein (B) in the porcine conceptuses/trophoblasts at different stages of development. The representative samples of Western blots are shown in the upper panels. Data are represented as the mean  $\pm$  SEM. Bars with different letter differ significantly ( $p<0.05$ ).

117x271mm (600 x 600 DPI)

FIGURE 2

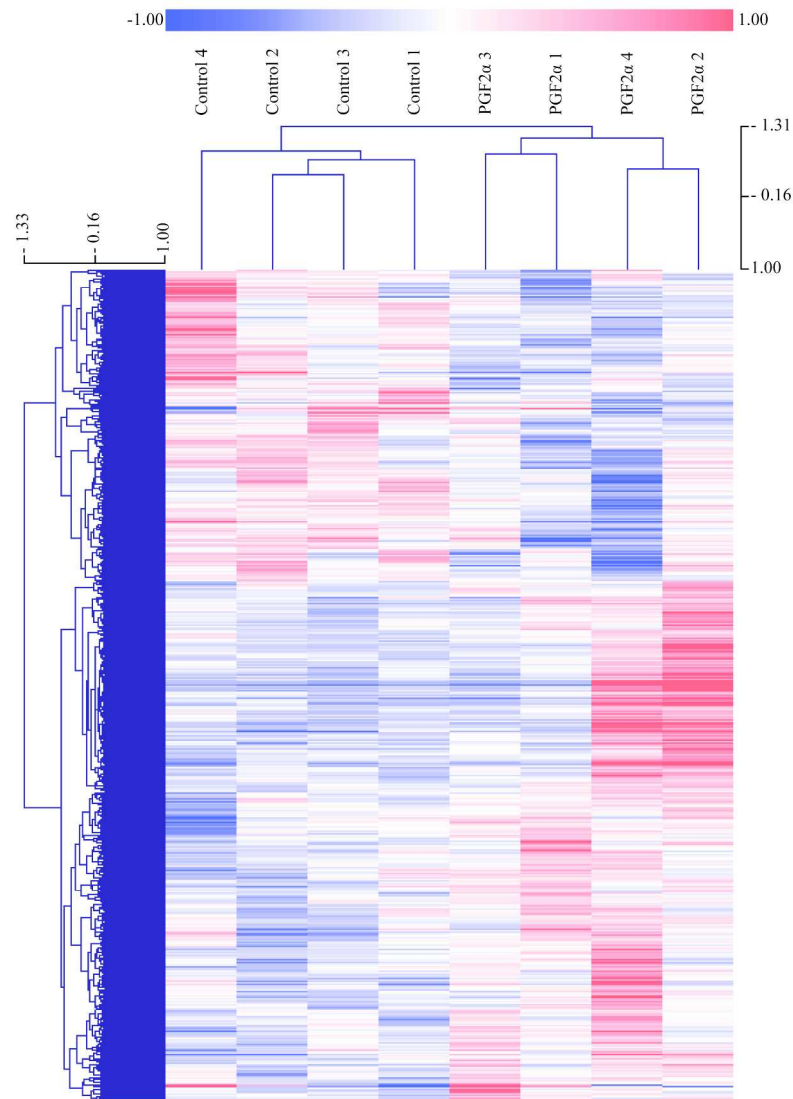


Figure 2. Heatmap showing microarray analysis of DEGs in PGF2 $\alpha$ -treated porcine trophoblast cells (PGF2 $\alpha$  1-4), and corresponding vehicle-treated controls (Control 1-4). Normalized expression data was clustered based on pair wise Pearson correlation using identified DEGs (red: correlation=1; blue: correlation= -1). 576 genes were differentially expressed between the two groups. A total of 360 genes were up-regulated and 216 genes were down-regulated ( $p < 0.05$ ). The full list of DEGs is provided in Supplementary Table 3.

196x290mm (300 x 300 DPI)

FIGURE 3

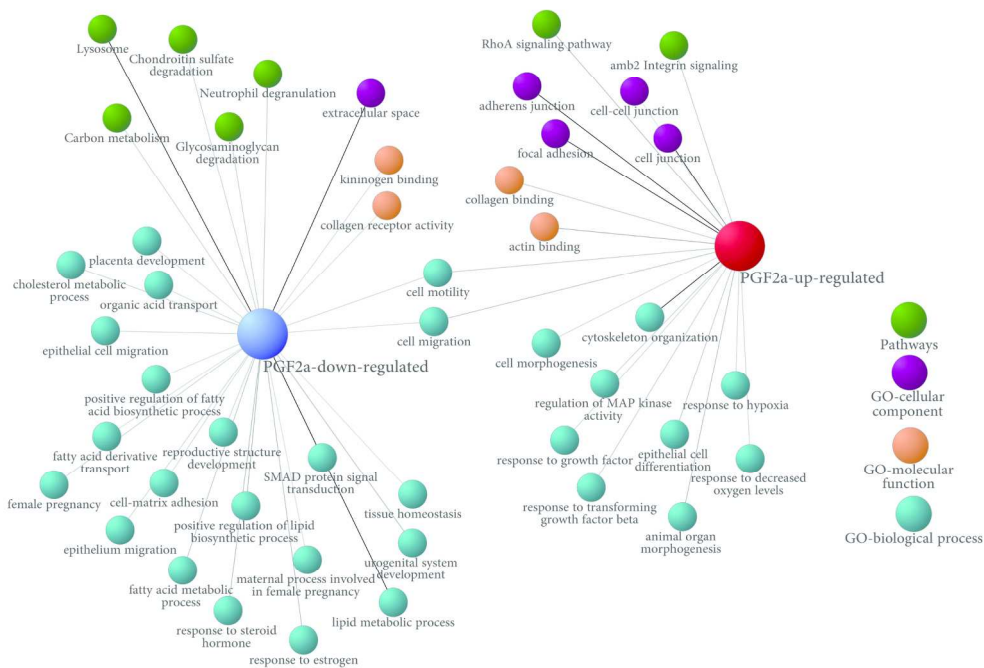


Figure 3. Functional map showing shared and treatment-specific functional annotation terms generated in multi-cluster gene functional enrichment analysis for DEGs identified in porcine primary trophoblast cells treated with PGF2 $\alpha$  or vehicle (control). Analysis was performed in ToppCluster software, functional map was edited and adjusted using Cytoscape. The redundant and non-informative terms were removed. Complete results are presented in tabular format in Supplementary Table 8.

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FIGURE 4

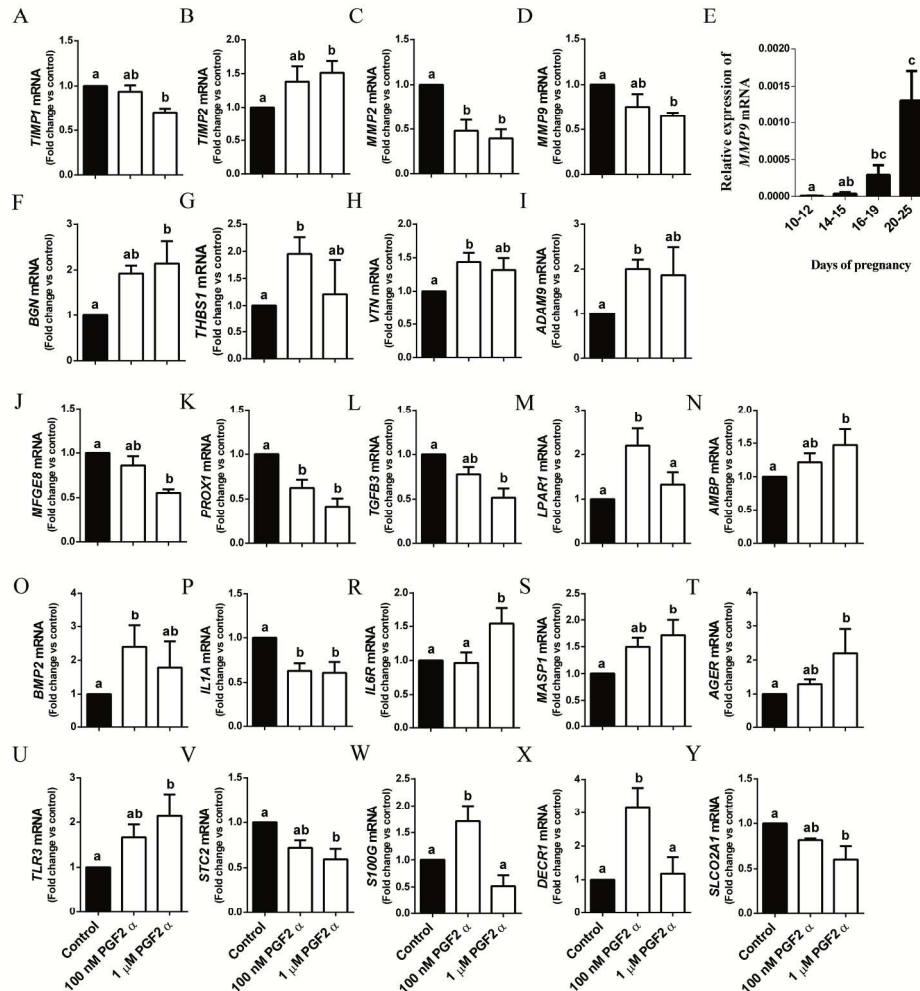


Figure 4. Expression of selected target genes determined by quantitative (real-time) RT-PCR in porcine primary trophoblast cells treated with PGF2 $\alpha$  (100 nM, 1  $\mu$ M) or vehicle (control). (A-D, F-Y). TIMP1-metalloproteinase inhibitor 1, TIMP2-metalloproteinase inhibitor 2, MMP2-matrix metalloproteinase 2, MMP9-matrix metalloproteinase 9, BGN-biglycan, THBS1-thrombospondin 1, VTN-vitronectin, ADAM9-ADAM metalloproteinase domain 9, MFGE8-milk fat globule-EGF factor 8 protein, PROX1-prospero homeobox 1, TGFB3-transforming growth factor beta 3, LPAR1-lysophosphatidic acid receptor 1, AMBP-alpha-1-microglobulin/bikunin precursor, BMP2-bone morphogenetic protein 2, IL1A-interleukin 1 alpha, IL6R-interleukin 6 receptor, MASP1-mannan binding lectin serine peptidase 1, AGER-advanced glycosylation end-product specific receptor, TLR3-toll-like receptor 3, STC2-stanniocalcin 2, S100G-S100 calcium binding protein G, DECRL-2,4-dienoyl-CoA reductase 1, SLCO2A1-solute carrier organic anion transporter family member 2A1. Expression of MMP9 mRNA in the porcine conceptuses/ trophoblasts at different stages of development (E). Data on panels A-D and F-Y are presented as means  $\pm$  SEM of fold change versus control (vehicle). Data on panel E is presented as mean  $\pm$  SEM. Bars with different letter differ significantly (p < 0.05).

205x224mm (300 x 300 DPI)





**FIGURE 5**

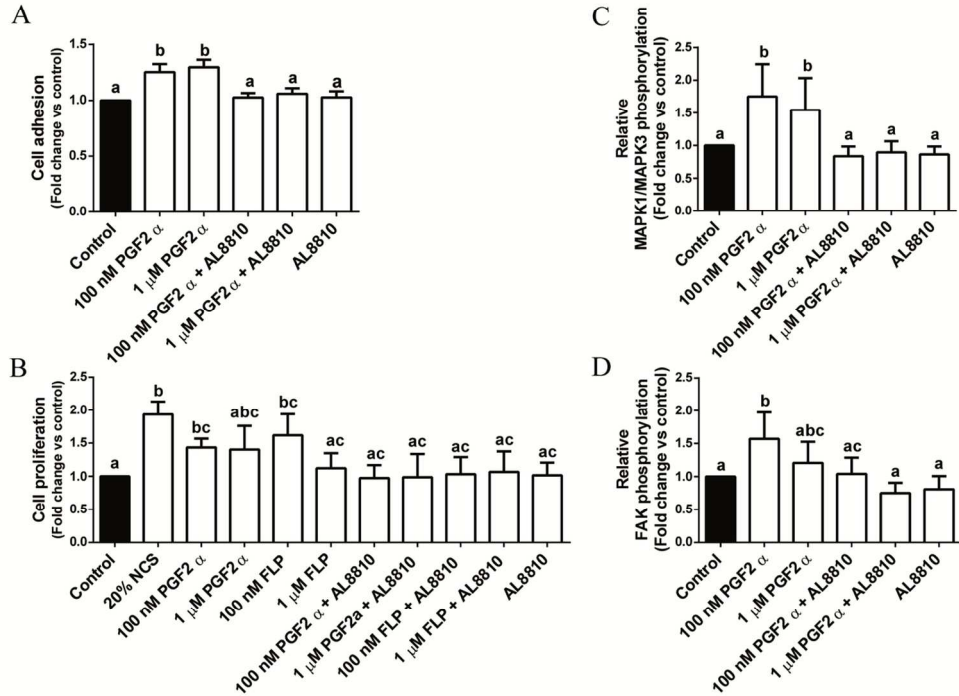


Figure 5. PGF2 $\alpha$  increased adhesion to extracellular matrix protein - fibronectin (A) and proliferation (B) of primary porcine trophoblast cells. Effect of PGF2 $\alpha$  on MAPK1/3 (C) and FAK (D) phosphorylation in porcine primary trophoblast cells in vitro. NCS-newborn calf serum (used as a positive control), FLP – fluprostenol (stable prostaglandin F2 $\alpha$  analogue), AL8810 – PTGFR antagonist. Data are presented as means  $\pm$  SEM of fold change versus control (vehicle). Different letters (a-c) indicate statistically significant differences ( $p < 0.05$ ).

121x97mm (300 x 300 DPI)

**Table 1. Primer sequences and assays used in qPCR analyses.**

Gene	Primer Sequence / TaqMan® Assay ID	RefSeq ID / GenBank Accession No.	Reference
<i>PTGFR</i>	sense: 5'-TCAGCAGCACAGACAAGG-3' antisense: 5'-TTCACAGGCATCCAGATAATC-3'	NM_214059	Kaczynski & Wacławik 2013
<i>ACTB</i>	Sense: 5'-ACATCAAGGAGAAGCTCTGCTACG-3' Antisense: 5'-GAGGGGCGATGATCTTGATCTTCA-3'	U07786	Kaczynski & Wacławik 2013
<i>GAPDH</i>	Sense: 5'-CAGCAATGCCTCCTGTACCA-3' Antisense: 5-GATGCCGAAGTTGTCATGGA-3'	AF017079	Kaczynski & Wacławik 2013
<i>PPIA</i>	Sense: 5'-TAACCCACCGTCTTCTT-3' Antisense: 5'-TGCCATCCAACCACTCAG-3'	AY266299.1	Kaczynski & Wacławik 2013
<i>ADAM9</i>	Ss03373282_m1	AF069646.1	-
<i>AGER</i>	Ss03390846_g1	EU282357.1	-
<i>AMBP</i>	Ss03374771_m1	AK232748.1	-
<i>BGN</i>	Ss03375454_u1	AF159382.1	Kaczynski <i>et al.</i> 2016
<i>BMP2</i>	Ss03373798_g1	AY669080	-
<i>DECR1</i>	Ss01051816_m1	AK230726.1	-
<i>IL1A</i>	Ss03391335_m1	X52731.1	Kaczynski <i>et al.</i> 2016
<i>IL6</i>	Ss03384604_u1	AF309651.1	Kaczynski <i>et al.</i> 2016
<i>KNG1</i>	Ss03373690_m1	AY321363.1	-
<i>LPAR1</i>	Ss03377225_u1	AK344044.1	-
<i>MASP1</i>	Ss04246770_m1	GU810082.1	-
<i>MFGE8</i>	Ss03390111_m1	AK233926.1	-
<i>MMP2</i>	Ss03394318_m1	AF295805.1	-
<i>MMP9</i>	Ss03392100_m1	DQ132879.1	Kaczynski <i>et al.</i> 2016
<i>PROX1</i>	Ss04246028_m1	EF486324.1	-
<i>SI00G</i>	Ss03382848_u1	L13068.1	-
<i>SLCO2A1</i>	Ss03390713_m1	NM_001123195	-
<i>STC2</i>	Ss03389624_m1	AK349078.1	-
<i>TGFB3</i>	Ss03394352_m1	X14150.1	Kaczynski <i>et al.</i> 2016
<i>THBS1</i>	Ss03373620_m1	AM238691.1	-
<i>TLR3</i>	Ss03388861_m1	AB111939.1	-
<i>VTN</i>	Ss03382603_u1	AK232304.1	-
<i>ACTB</i>	Ss03376081_u1	AK237086.1	Kaczynski <i>et al.</i> 2016
<i>PPIA</i>	Ss03394782_g1	AY266299.1	Kaczynski <i>et al.</i> 2016
<i>GAPDH</i>	Ss03375435_u1	NM_001206359.1	Kaczynski <i>et al.</i> 2016

**Table 2. List of antibodies used in Western Blot analyses and immunolocalization experiments.**

<b>Peptide/Protein Target</b>	<b>Antigen Sequence</b>	<b>Name of Antibody</b>	<b>Manufacturer, Catalog No., or Name of Source</b>	<b>Species Raised in Monoclonal or Polyclonal</b>	<b>Dilution used</b>
PTGFR	QRFRQKSKASFLLLASGLVITDFFGHLI NGAIAVFVYASDKEWIRFDQSNVLCIS	PGF2aR antibody (H-55)	Santa Cruz Biotechnology, sc-67029	Rabbit, polyclonal	1:50
MAPK1/3	N/A	p44/42 MAPK (Erk1/2) antibody	Cell Signaling, #9102S	Rabbit, polyclonal	1:300
phospho-MAPK1/3	N/A	Phospho-p44/42 MAPK (Erk1/2) (Thr202/Tyr204) antibody	Cell Signaling, #9101	Rabbit, polyclonal	1:300
FAK	N/A	Focal Adhesion Kinase (FAK) antibody	Cell Signaling, #3285S	Rabbit, polyclonal	1:300
phospho-FAK	N/A	Phospho-FAK (Tyr397) antibody	Cell Signaling, #3283	Rabbit, polyclonal	1:300
Cytokeratin	N/A	Anti-Pan Cytokeratin antibody	Sigma-Aldrich C 9687	Mouse monoclonal	1:50
anti-rabbit HRP	N/A	Immun-Star™ Goat Anti-Rabbit (GAR)-HRP Conjugate	Bio-Rad Laboratories, #170-5046	Goat, polyclonal	1:20000
anti-mouse	N/A	Cy™3 AffiniPure Donkey Anti-Mouse IgG	Jackson ImmunoResearch # 715-165-150	Donkey, polyclonal	1:1000

**Table 3. Selected results of DAVID functional annotation clustering for differentially expressed genes in trophoblast cells treated with PGF2 $\alpha$ .**

<b>Selected functional terms of overrepresented annotation clusters</b>	<b>Enrichment score</b>
<b>UP REGULATED</b>	
focal adhesion (30; 3.67); cell adhesion (50; 1.48); protein binding involved in cell adhesion (14; 2.29)	3.96
cell migration (42; 1.79); regulation of cell motility (28; 1.91)	2.91
response to hypoxia (17; 3.01)	2.84
response to fibroblast growth factor (10; 3.71); fibroblast growth factor receptor signaling pathway (8; 4.01)	2.53
response to growth factor (28; 2.23); response to transforming growth factor beta (13; 3.05); transmembrane receptor protein serine/threonine kinase signaling pathway (14; 2.19)	2.43
regulation of cell proliferation (19; 1.50)	2.32
response to steroid hormone (16; 2.11)	2.26
anatomical structure formation involved in morphogenesis (38; 1.67); angiogenesis (17; 2.07)	2.01
regulation of MAP kinase activity (18; 2.78); protein phosphorylation (50; 1.36)	1.95
regulation of epithelial cell proliferation (14; 2.35)	1.68
organ morphogenesis (36; 1.83); epithelium development (32; 1.52)	1.52
extracellular matrix binding (5; 4.72)	1.35
<b>DOWN REGULATED</b>	
fatty acid biosynthetic process (6; 3.38)	2.71
regulation of intracellular signal transduction (34; 1.62)	2.04
steroid biosynthetic process (7; 3.91)	1.89
cell migration (28; 1.93)	1.85
anion transport (14; 2.44)	1.79
regulation of cell proliferation (31; 1.63)	1.78
extracellular matrix organization (11; 2.69)	1.74
female pregnancy (8; 3.49)	1.65
cellular response to interferon gamma (6; 3.63)	1.34
placenta development (6; 3.38); reproductive structure development (11; 2.15)	1.35